

SCORE Search Results Details for Application 10502115 and Search Result 20070517_165827_us-10-502-115- 1_copy_17_22.rag.

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OM protein - protein search, using sw model

Run on: May 18, 2007, 23:39:41 ; Search time 212 Seconds
(without alignments)
13.859 Million cell updates/sec

Title: US-10-502-115-1_COPY_17_22
Perfect score: 29
Sequence: 1 LKKTET 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a

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OM protein - protein search, using sw model

Run on: May 18, 2007, 23:39:41 ; Search time 247 Seconds
(without alignments)
13.859 Million cell updates/sec

Title: US-10-502-115-1_COPY_17_23
Perfect score: 34
Sequence: 1 LKKTETQ 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a

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OM protein - protein search, using sw model

Run on: May 18, 2007, 23:41:50 ; Search time 213 Seconds
(without alignments)
30.168 Million cell updates/sec

Title: US-10-502-115-1_COPY_17_22
Perfect score: 29
Sequence: 1 LKKTET 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_8.4:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	38	2 Q27I67_9HYST	Q27i67 bathyergus

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OM protein - protein search, using sw model

Run on: May 18, 2007, 23:41:50 ; Search time 249 Seconds
(without alignments)
30.168 Million cell updates/sec

Title: US-10-502-115-1_COPY_17_23
Perfect score: 34
Sequence: 1 LKKTETQ 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_8.4:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	34	100.0	38	2	Q27I67_9HYST	Q27i67 bathyergus

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OM protein - protein search, using sw model

Run on: May 18, 2007, 23:50:00 ; Search time 23 Seconds
(without alignments)
25.527 Million cell updates/sec

Title: US-10-502-115-1_COPY_17_22

Perfect score: 29

Sequence: 1 LKKTET 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query				Description
			Match	Length	DB	ID	
	1	29	100.0	40	2	A59005	thymosin beta - se
	2	29	100.0	40	2	B59005	thymosin beta - sc
	3	29	100.0	41	1	A60290	thymosin beta-9-Me
	4	29	100.0	41	2	B19438	thymosin beta-9 -
	5	29	100.0	43	1	TNBOB4	thymosin beta-4 -
	6	29	100.0	43	2	S21282	thymosin beta-11 -
	7	29	100.0	43	2	S21694	thymosin beta-12 -

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OM protein - protein search, using sw model

Run on: May 18, 2007, 23:50:00 ; Search time 26 Seconds
(without alignments)
25.527 Million cell updates/sec

Title: US-10-502-115-1_COPY_17_23

Perfect score: 34

Sequence: 1 LKKTETQ 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	34	100.0	40	2	A59005	thymosin beta - se
2	34	100.0	41	1	A60290	thymosin beta-9-Me
3	34	100.0	41	2	B19438	thymosin beta-9 -
4	34	100.0	43	1	TNBOB4	thymosin beta-4 -
5	34	100.0	43	2	S21282	thymosin beta-11 -
6	34	100.0	43	2	S21694	thymosin beta-12 -
7	34	100.0	44	1	A38682	thymosin beta-4 [v

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OM protein - protein search, using sw model

Run on: May 18, 2007, 23:57:45 ; Search time 34 Seconds
(without alignments)
15.377 Million cell updates/sec

Title: US-10-502-115-1_COPY_17_22
Perfect score: 29
Sequence: 1 LKKTET 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: May 18, 2007, 23:57:45 ; Search time 40 Seconds
(without alignments)
15.377 Million cell updates/sec

Title: US-10-502-115-1_COPY_17_23
Perfect score: 34
Sequence: 1 LKKTETQ 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search; using sw model

Run on: May 18, 2007, 23:58:26 ; Search time 121 Seconds
(without alignments)
22.984 Million cell updates/sec

Title: US-10-502-115-1_COPY_17_22
Perfect score: 29
Sequence: 1 LKKTET 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: May 18, 2007, 23:58:26 ; Search time 141 Seconds
(without alignments)
22.984 Million cell updates/sec

Title: US-10-502-115-1_COPY_17_23
Perfect score: 34
Sequence: 1 LKKTETQ 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

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OM protein - protein search, using sw model

Run on: May 18, 2007, 23:59:47 ; Search time 82 Seconds
(without alignments)
22.857 Million cell updates/sec

Title: US-10-502-115-1_COPY_17_22
Perfect score: 29
Sequence: 1 LKKTET 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1301799 seqs, 311203995 residues

Total number of hits satisfying chosen parameters: 1301799

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: May 18, 2007, 23:59:47 ; Search time 95 Seconds
(without alignments)
22.857 Million cell updates/sec

Title: US-10-502-115-1_COPY_17_23
Perfect score: 34
Sequence: 1 LKKTETQ 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1301799 seqs, 311203995 residues

Total number of hits satisfying chosen parameters: 1301799

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.